IN THE SPECIFICATION

Please **add** the following paragraph on page 1, line 3 following the Title of the application and prior to the section entitled "Cross Reference to Related Applications":

INCORPORATION OF SEQUENCE LISTING

D1

A paper copy of the Sequence Listing and a computer readable form of the sequence listing on diskette, containing the file named "Seq listing for tocopherol nonprovisional.txt", which is 304,878 bytes in size (measured in MS-DOS), and which was created on March 12, 1999, are herein incorporated by reference.

On page 16, lines 10-20, please **delete** the paragraph beginning "[s]imilarity analysis includes database...". Please **add** the following paragraph on page 16 in place of the deleted paragraph:

D2

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) **(www-ddbj.nig.ac.jp/)** ~~(http://www.ddbj.nig.ac.jp/)~~; Genebank **(www-ncbi.nlm.nih.gov/Web/Search/Index.htlm)** ~~(http://www.ncbi.nlm.nih.gov/Web/Search/Index.htlm)~~; and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) **(www-ebi.ac.uk/ebi_docs/embl_db/embl-db.htlm)** ~~(http://www.ebi.ac.uk/ebi_docs/embl_db/embl-db.html)~~. A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12:* 76-80 (1994); Birren, *et al., Genome Analysis, 1:* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York 543-559 (1997)).